

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (currently amended): An isolated protein comprising:
 - a) the 4- α -helix bundle motif formed from the α -helices of the ROP (repressor of primer) of SEQ ID NO:11 and
 - b) a redox centre,
wherein the redox centre comprises a metal atom which is stable in different oxidation states.
2. (previously presented): The protein of Claim 1, wherein the redox centre comprises a metal atom which is stable in two different oxidation states.
3. (previously presented): The protein of Claim 1, wherein the redox centre is bound to the protein, by coordination by one or more of histidine, leucine, methionine or cysteine residues.
4. (previously presented): The protein of Claim 1, wherein the redox centre is covalently bound to the 4- α -helix bundle motif formed from the α -helices of ROP.
5. (original): The protein of Claim 1 which has a redox mid-point potential in the range of -485 to +320mV.

6. (withdrawn-currently amended): The protein of Claim 1 which has α -helix regions each having at least 60% similarity or identity with the α -helix regions of ~~sequence~~ SEQ ID Nos. 1 and 3.

7. (withdrawn): The protein of claim 6, wherein said four α -helix regions are connected by loops.

8. (withdrawn): The protein of claim 7, wherein the four α -helices are joined in the order 1-1'-2'-2.

9. (withdrawn-currently amended): The protein of Claim 1 which is formed by connecting two wild type ROP proteins to obtain the 4-helix bundle as one continuous polypeptide having at least 60% similarity or identity with ~~sequence~~ SEQ ID No. 8.

10. (withdrawn): The protein of claim 9, wherein the histidine residues corresponding to H76, H78, H107 and H109 in sequence ID No. 8 are removed.

11. (withdrawn-currently amended): The protein of claim 9, wherein histidine, leucine, methionine or cysteine residues are introduced one or both positions corresponding to 56 and 113 in ~~sequence~~ SEQ ID No. 8.

12. (previously presented): The protein of claim 1 which has a haem redox centre coordinated to the 4- α -helix bundle motif via two histidine residues.

13. (original): The protein of claim 12 which has a mid-point potential in the range -400mV to +300MV.

14. (currently amended): The protein of claim 12 which has the sequence as indicated by ~~sequence~~ SEQ ID No.: 11.

15. (previously presented): The protein of claim 1 which has a stability, measured as the unfolding free energy when denaturant is added to the protein of $\Delta G_{\text{obs}}\text{H}_2\text{O}$ is greater than or equal to y, wherein y is greater than or equal to 3.0 kcal/mol.

16. (withdrawn): A method of producing the protein of claim 1 comprising
- i) expressing all four α -helices as a single polypeptide chain;
 - ii) engineering the required mutations to enable redox centre binding;
 - iii) expressing and purifying, or producing the redox centre binding mutant;
- and
- iv) incubating the mutant with an excess of the redox centre to produce the protein.

17. (withdrawn): A nucleotide sequence which encodes the protein of claim 1 or a fragment thereof.

18. (withdrawn): A vector comprising the nucleotide sequence of claim 17.
19. (canceled).
20. (withdrawn): A method of passing electrons along a sequence of electron carriers, in which each electron carrier is reduced and then oxidized or vice versa by electron movement and the sequence of electron carriers includes the protein of claim 1.
21. (previously presented): An apparatus comprising the protein of claim 1 associated with the electrode.
22. (original): An apparatus according to claim 21 wherein the protein is absorbed onto an electrode.
23. (withdrawn): A protein according to claim 2 in which the redox centre is an iron sulfur centre.
- 24.-25. (canceled).
26. (withdrawn-currently amended): A protein according to claim 6 in which the α -helix regions each have at least 80% similarity or identity with the α -helix regions of ~~sequence~~ SEQ ID No. 1.

27. (withdrawn-currently amended): A protein according to claim 9 in which the continuous polypeptide has at least 80% similarity or identity with ~~sequence~~ SEQ ID No.: 8.